



Attorney Docket No.: 08411-032001 / ISURF 02410-P1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David A. Wright et al.

Art Unit : 1636 /

Serial No. : 09/586,106

Examiner : Konstantina T. Katcheves

Filed : June 2, 2000

Title : PLANT RETROELEMENTS AND METHODS RELATED THERETO

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Commissioner for Patents

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REPLY

This communication is in reply to the action mailed May 7, 2003. Applicant asks that claims 1-4, 9-12, 15-18, 21-23, and 25-33 be allowed in view of the remarks contained on the following pages, a total of 9 sheets.

Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: August 7, 2003

Elizabeth N. Kaytor  
Elizabeth N. Kaytor, Ph.D.  
Reg. No. 53,103

Fish & Richardson P.C., P.A.  
60 South Sixth Street  
Suite 3300  
Minneapolis, MN 55402  
Telephone: (612) 335-5070  
Facsimile: (612) 288-9696

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Theresa Brehm

In the claims:

Please amend the claims as follows:

1. (Previously amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) a sequence having more than 85% identity to SEQ ID NO 62;
- (b) a sequence encoding a polypeptide comprising an amino acid sequence having more than 85% identity to SEQ ID NO 63; and
- (c) a sequence fully complementary to (a) or (b).

2. (Currently amended) A transformed seed containing a ~~recombination~~ recombinant construct comprising [[a]] the nucleic acid of claim 1.

3. (Currently amended) A transformed plant containing a ~~recombination~~ recombinant construct comprising [[a]] the nucleic acid of claim 1.

4. (Previously amended) The nucleic acid molecule of claim 26, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.

5-8. (Cancelled)

9. (Previously amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) a sequence having more than 95% identity to SEQ ID NO 62;
- (b) a sequence encoding a polypeptide comprising an amino acid sequence having more than 95% identity to SEQ ID NO 63; and
- (c) a sequence fully complementary to (a) or (b).

10. (Currently amended) A transformed seed containing a ~~recombination~~ recombinant construct comprising [[a]] the nucleic acid of claim 9.

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11. (Currently amended) A transformed plant containing a ~~recombination~~  
recombinant construct comprising ~~[[a]] the~~ nucleic acid of claim 9.

12. (Previously amended) The nucleic acid molecule of claim 27, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.

13-14. (Cancelled)

15. (Previously amended) The nucleic acid molecule of claim 9, wherein said nucleic acid molecule comprises a nucleic acid sequence having 100% identity to SEQ ID NO:62.

16. (Currently amended) A transformed seed containing a ~~recombination~~  
recombinant construct comprising ~~[[a]] the~~ nucleic acid of claim 15.

17. (Currently amended) A transformed plant containing a ~~recombination~~  
recombinant construct comprising ~~[[a]] the~~ nucleic acid of claim 15.

18. (Previously amended) The nucleic acid molecule of claim 33, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.

19-20. (Cancelled)

21. (Previously amended) The nucleic acid of claim 15, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.

22. (Previously amended) The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance; improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.

23. (Previously amended) The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.

24. (Cancelled)

25. (Previously amended) The plant of claim 17, which plant is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; cabbage; oat; rye; cotton; flax; potato; pine; walnut; citrus; hemp; oak; rice; petunia; orchids; Arabidopsis; broccoli; cauliflower; brussel sprouts; onion; garlic; leek; squash; pumpkin; celery; pea; bean; strawberries; grapes; apples; pears; peaches; banana; palm; cocoa; cucumber; pineapple; apricot; plum; sugar beet; lawn grasses; maple; triticale; safflower; peanut; and olive.

26. (Previously added) The nucleic acid of claim 1, wherein a pol coding sequence comprises said nucleic acid.

27. (Previously added) The nucleic acid of claim 9, wherein a pol coding sequence comprises said nucleic acid.

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28. (Previously added) The nucleic acid molecule of claim 9, wherein said nucleic acid molecule encodes a polypeptide having an amino acid sequence with 100% identity to SEQ ID NO:63.

29. (Currently amended) A transformed seed containing a ~~recombination~~ recombinant construct comprising the nucleic acid of claim 28.

30. (Currently amended) A transformed plant containing a ~~recombination~~ recombinant construct comprising the nucleic acid of claim 28.

31. (Previously added) The nucleic acid of claim 28, wherein a pol coding sequence comprises said nucleic acid.

32. (Previously added) The nucleic acid of claim 31, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.

33. (Previously added) The nucleic acid of claim 15, wherein a pol coding sequence comprises said nucleic acid.